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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=12; day=17; hr=11; min=8; sec=3; ms=26;]

=====

Reviewer Comments:

<210> 10

<211> 519

<212> PRT

<213> *Physcomitrella patens*

<400> 10

Met	Thr	Ser	Thr	Glu	Asn	Thr	Ala	Met	Phe	Thr	Glu	Asp	Thr	Ser	Thr
1				5				10						15	
Leu	Asn	Gly	Ser	Thr	Glu	Ala	Asn	His	Ala	Glu	Phe	Pro	Leu	Gly	Glu
				20				25						30	
Arg	Pro	Thr	Ile	Gly	Pro	Glu	Pro	Pro	Val	Asn	Pro	Phe	His	Glu	Ser
				35				40						45	
Ser	Thr	Trp	Ser	Ile	Pro	Gln	Val	Ile	Lys	Thr	Ile	Leu	Leu	Val	Pro
				50				55						60	
Leu	Leu	Val	Ile	Arg	Leu	Leu	Ser	Met	Phe	Ala	Leu	Met	Met	Leu	Gly
65					70					75					80
Tyr	Ile	Cys	Val	Lys	Val	Ala	Met	Ile	Gly	Cys	Lys	Asp	Pro	Leu	Phe
				85						90					95
Lys	Pro	Phe	Asn	Pro	Leu	Arg	Arg	Leu	Leu	Leu	Val	Ser	Val	Arg	Leu
				100						105					110
Ile	Ala	Arg	Gly	Val	Met	Val	Ala	Met	Gly	Tyr	Tyr	Tyr	Ile	Leu	Val
				115						120					125
Lys	Gly	Lys	Pro	Ala	His	Arg	Ser	Val	Ala	Pro	Ile	Ile	Val	Ser	Asn
				130						135					140
His	Ile	Gly	Phe	Val	Asp	Pro	Ile	Phe	Val	Phe	Tyr	Arg	His	Leu	Pro
145					150					155					160
Val	Ile	Val	Ser	Ala	Lys	Glu	Ile	Val	Glu	Met	Pro	Ile	Ile	Gly	Met
				165						170					175
Phe	Leu	Gln	Ala	Leu	Gln	Ile	Ile	Pro	Val	Asp	Arg	Ile	Asn	Pro	Ala

Ser Arg His His Ala Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn
195 200 205
Glu Trp Pro His Val Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly

In the above attachment, please delete the extra space between the bases. This type of error is seen globally throughout the sequences in the sequence listing.

<210> 56
<211> 17752
<212> DNA

<213> Artificial sequence

<220>

<223> Vector comprising genes coding for Physcomitrella patens Delta-6-elongase, Physcomitrella patens Delta-6-desaturase, and Phaeodactylum tricornutum Delta-5-desaturase

Invalid Line Length in Numeric Identifier <223>, The rules require that a line not exceed 72 characters in length. This includes white spaces. Please check for similar errors and make necessary changes.

Application No: 10552013 Version No: 3.0

Input Set:

Output Set:

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Started:      2009-11-23 16:16:35.058
Finished:    2009-11-23 16:16:53.988
Elapsed:      0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors:  202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

```

[illegible]

Input Set:

Output Set:

Started: 2009-11-23 16:16:35.058
Finished: 2009-11-23 16:16:53.988
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors: 202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 300	Invalid codon found Met SEQID (9) POS: 920
E 300	Invalid codon found Leu SEQID (9) POS: 923
E 300	Invalid codon found Phe SEQID (9) POS: 926
E 300	Invalid codon found Pro SEQID (9) POS: 929
E 300	Invalid codon found Glu SEQID (9) POS: 932
E 300	Invalid codon found Gly SEQID (9) POS: 935
E 300	Invalid codon found Thr SEQID (9) POS: 938
E 300	Invalid codon found Thr SEQID (9) POS: 941
E 300	Invalid codon found Thr SEQID (9) POS: 944
E 300	Invalid codon found Asn SEQID (9) POS: 947
E 300	Invalid codon found Gly SEQID (9) POS: 950
E 300	Invalid codon found Lys SEQID (9) POS: 953
E 300	Invalid codon found Ala SEQID (9) POS: 956
E 300	Invalid codon found Leu SEQID (9) POS: 959
E 300	Invalid codon found Ile SEQID (9) POS: 962
E 300	Invalid codon found Ser SEQID (9) POS: 965
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 300	Invalid codon found Lys SEQID (11) POS: 961
E 300	Invalid codon found Ala SEQID (11) POS: 964

Input Set:

Output Set:

Started: 2009-11-23 16:16:35.058
Finished: 2009-11-23 16:16:53.988
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors: 202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 300	Invalid codon found Asn SEQID (11) POS: 967
E 300	Invalid codon found Gln SEQID (11) POS: 970 This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

Input Set:

Output Set:

Started: 2009-11-23 16:16:35.058
Finished: 2009-11-23 16:16:53.988
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors: 202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (37)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 213	Artificial or Unknown found in <213> in SEQ ID (56)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)

Input Set:

Output Set:

Started: 2009-11-23 16:16:35.058
Finished: 2009-11-23 16:16:53.988
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors: 202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 213	Artificial or Unknown found in <213> in SEQ ID (71)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (71)
W 213	Artificial or Unknown found in <213> in SEQ ID (75)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)

Input Set:

Output Set:

Started: 2009-11-23 16:16:35.058
Finished: 2009-11-23 16:16:53.988
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings: 103
Total Errors: 202
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89)

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
 Sozer, Nursen
 Frentzen, Margit
 Bauer, Jorg
 Keith, Stobart
 Fraser, Thomas
 Lazarus, Colin M
 Qi, Baoxiu
 Abbadi, Amine
 Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
 UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013

<141> 2005-09-30

<150> PCT/EP2004/003224

<151> 2004-03-26

<150> DE103 14 759.4

<151> 2003-03-31

<150> DE103 48 996.7

<151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1

<211> 1047

<212> DNA

<213> Thraustochytrium

<220>

<221> CDS

<222> (38)..(952)

<223> LPAAT

<400> 1

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                                1             5

gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg      103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
                                10             15             20

ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc      151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
                                25             30             35

acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc      199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

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40	45	50	
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc			247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val			
55	60	65	70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg			295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala			
75	80	85	
aac cac gtc tgc tac ctg gag atc ttg tac ttc atg tgc acc gtg cac			343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His			
90	95	100	
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc			391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val			
105	110	115	
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc			439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly			
120	125	130	
ggc ggt caa agc gca tgc gcg atc att cgc gac cgc gtg cag gag cct			487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro			
135	140	145	150
cct cga gat tgc tgc agc gag aag cac cac gcg cag ccg ctt ctt gtg			535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val			
155	160	165	
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag			583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys			
170	175	180	
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag			631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu			
185	190	195	
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tgc			679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser			
200	205	210	
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac			727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His			
215	220	225	230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag			775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu			
235	240	245	
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg			823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala			
250	255	260	
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc			871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu			
265	270	275	
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga			919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly			
280	285	290	
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca			972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu			
295	300	305	
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aaaaaaaaaa aaaaaa			1047

<210> 2

<211> 305

<212> PRT

<213> Thraustochytrium

<400> 2

Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
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20 25 30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
35 40 45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
50 55 60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65 70 75 80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
85 90 95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
100 105 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
115 120 125
Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
130 135 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145 150 155 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
165 170 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
180 185 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
195 200 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
210 215 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225 230 235 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
245 250 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
260 265 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
275 280 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
290 295 300
Leu
305

<210> 3

<211> 1701

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> misc_feature

<223> LPAAT

<400> 3

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tttgcaattt tcttttgctg ttaacctatt gatttatgtg gaaccacaat acagacgctg 300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggtaattt catcctacag 360
ggatatggat gttgtaaagg tgatttttgc aggtgataaa gtacctaaagg agaaccgtgt 420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttga acttagcaat 480
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cttgtttggg tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt 600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg 660
gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtacc atccatggct 720
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gagaaaggct atccggagct tgtcaatgtg cttcaacctc gactcgtgg ctttgtgact 960
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taagetgatt tttgctatta attggctgct ccttggtttg tctgcgtaaa attggcttta 1560
atacggttgt cttctgctga tgaacctcag tgcctcaaga cgatgtggcc ttttagcctt 1620
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<210> 4
<211> 714
<212> DNA
<213> Physcomitrella patens

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<220>
<221> CDS
<222> (1)..(714)
<223> LPAAT

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tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc 96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
20 25 30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat 144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
35 40 45
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa 192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
50 55 60
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt 240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65 70 75 80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac 288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp

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85	90	95	
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Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
100	105	110	
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca			384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro			
115	120	125	
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat			432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca			480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
145	150	155	160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg			528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta			576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val			
180	185	190	
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc			624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe			
195	200	205	
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa			672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys			
210	215	220	
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa			714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val			
225	230	235	

<210> 5

<211> 237

<212> PRT

<213> Physcomitrella patens

<400> 5

Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe			
1	5	10	15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser			
20	25	30	
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr			
35	40	45	
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys			
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Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe			
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Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp			
85	90	95	
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
100	105	110	
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro			
115	120	125	
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
145	150	155	160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	

Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
180 185 190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
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Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
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Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
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Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
20 25 30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc 144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
35 40 45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg 192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
50 55 60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg 240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65 70 75 80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc 288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile

85

90

95

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336